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RAW SEQUENCE LISTING   DATE: 01/23/2002
PATENT APPLICATION: US/09/754,014   TIME: 14:37:02

Input Set : **N:\Crf3\RULE60\09754014.raw**
Output Set: **N:\CRF3\01232002\I754014.raw**

SEQUENCE LISTING
```
  3 (1) GENERAL INFORMATION:
  6      (i) APPLICANT: Jeff Nordstrom
  7                     Bruce Freimark
  8                     Deepa Deshpande
 11    (ii) TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYTEMS
 12                             AND USES
 15   (iii) NUMBER OF SEQUENCES: 12
 18    (iv) CORRESPONDENCE ADDRESS:
 20         (A) ADDRESSEE: Lyon & Lyon
 21         (B) STREET: 633 West Fifth Street
 22                     Suite 4700
 23         (C) CITY: Los Angeles
 24         (D) STATE: California
 25         (E) COUNTRY: U.S.A.
 26         (F) ZIP: 90071-2066
 29     (v) COMPUTER READABLE FORM:
 31         (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 32                         storage
 33         (B) COMPUTER: IBM Compatible
 34         (C) OPERATING SYSTEM: IBM P.C. DOS 5.0
 35         (D) SOFTWARE: FastSEQ for Windows 2.0
 38    (vi) CURRENT APPLICATION DATA:
C--> 40     (A) APPLICATION NUMBER: US/09/754,014
C--> 41     (B) FILING DATE: 03-Jan-2001
 42         (C) CLASSIFICATION:
 45   (vii) PRIOR APPLICATION DATA:
 47         (A) APPLICATION NUMBER: 08/948,958
 48         (B) FILING DATE:
 51  (viii) ATTORNEY/AGENT INFORMATION:
 53         (A) NAME: Berkman, Charles S.
 54         (B) REGISTRATION NUMBER: 38,077
 55         (C) REFERENCE/DOCKET NUMBER: 226/284
 57    (ix) TELECOMMUNICATION INFORMATION:
 59         (A) TELEPHONE: (213) 489-1600
 60         (B) TELEFAX: (213) 955-0440
 61         (C) TELEX: 67-3510
 69 (2) INFORMATION FOR SEQ ID NO: 1:
 71     (i) SEQUENCE CHARACTERISTICS:
 73         (A) LENGTH: 328 amino acids
 74         (B) TYPE: amino acid
 75         (C) STRANDEDNESS: single
 76         (D) TOPOLOGY: linear
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ENTERED

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78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80    Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
81    1                   5                   10                  15
83    Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
84                    20                  25                  30
86    Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
87                    35                  40                  45
89    Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln
90        50                  55                  60
92    Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
93    65                  70                  75                  80
95    Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
96                    85                  90                  95
98    Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
99                    100                 105                 110
101   Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
102             115                 120                 125
104   Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
105       130                 135                 140
107   Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
108   145                 150                 155                 160
110   Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
111             165                 170                 175
113   Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
114             180                 185                 190
116   Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
117             195                 200                 205
119   Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
120       210                 215                 220
122   Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
123   225                 230                 235                 240
125   Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
126             245                 250                 255
128   Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
129             260                 265                 270
131   Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
132       275                 280                 285
134   Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
135       290                 295                 300
137   Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
138   305                 310                 315                 320
141   Glu Trp Ala Ser Val Pro Cys Ser
142                   325
146 (2) INFORMATION FOR SEQ ID NO: 2:
148         (i) SEQUENCE CHARACTERISTICS:
150             (A) LENGTH: 987 base pairs
151             (B) TYPE: nucleic acid
152             (C) STRANDEDNESS: single
153             (D) TOPOLOGY: linear
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155     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
157 ATGTGTCACC AGCAGTTGGT CATCTCTTGG TTTTCCCTGG TTTTTCTGGC ATCTCCCTC      60
158 GTGGCCATAT GGGAACTGAA GAAAGATGTT TATGTCGTAG AATTGGATTG GTATCCGGAT     120
159 GCCCCTGGAG AAATGGTGGT CCTCACCTGT GACACCCCTG AAGAAGATGG TATCACCTGG     180
160 ACCTTGGACC AGAGCAGTGA GGTCTTAGGC TCTGGCAAAA CCCTGACCAT CCAAGTCAAA     240
161 GAGTTTGGAG ATGCTGGCCA GTACACCTGT CACAAAGGAG GCGAGGTTCT AAGCCATTCG     300
162 CTCCTGCTGC TTCACAAAAA GGAAGATGGA ATTTGGTCCA CTGATATTTT AAAGGACCAG     360
163 AAAGAACCCA AAAATAAGAC CTTTCTAAGA TGCGAGGCCA AGAATTATTC TGGACGTTTC     420
164 ACCTGCTGGT GGCTGACGAC AATCAGTACT GATTTGACAT TCAGTGTCAA AAGCAGCAGA     480
165 GGCTCTTCTG ACCCCCAAGG GGTGACGTGC GGAGCTGCTA CACTCTCTGC AGAGAGAGTC     540
166 AGAGGGACA  ACAAGGAGTA TGAGTACTCA GTGGAGTGCC AGGAGGACAG TGCCTGCCCA     600
167 GCTGCTGAGG AGAGTCTGCC CATTGAGGTC ATGGTGGATG CCGTTCACAA GCTCAAGTAT     660
168 GAAAACTACA CCAGCAGCTT CTTCATCAGG GACATCATCA AACCTGACCC ACCCAAGAAC     720
169 TTGCAGCTGA AGCCATTAAA GAATTCTCGG CAGGTGGAGG TCAGCTGGGA GTACCCTGAC     780
170 ACCTGGAGTA CTCCACATTC CTACTTCTCC CTGACATTCT GCGTTCAGGT CCAGGGCAAG     840
171 AGCAAGAGAG AAAAGAAAGA TAGAGTCTTC ACGGACAAGA CCTCAGCCAC GGTCATCTGC     900
172 CGCAAAAATG CCAGCATTAG CGTGCGGGCC CAGGACCGCT ACTATAGCTC ATCTTGGAGC     960
173 GAATGGGCAT CTGTGCCCTG CAGTTAG                                         987
177 (2) INFORMATION FOR SEQ ID NO: 3:
179     (i) SEQUENCE CHARACTERISTICS:
181         (A) LENGTH: 987 base pairs
182         (B) TYPE: nucleic acid
183         (C) STRANDEDNESS: single
184         (D) TOPOLOGY: linear
186     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
188 ATGTGCCACC AGCAGCTGGT GATCAGCTGG TTCAGCCTGG TGTTCCTGGC CAGCCCCCTG      60
189 GTGGCCATCT GGGAGCTGAA GAAGGACGTG TACGTGGTGG AGCTGGACTG GTACCCCGAC     120
190 GCCCCCGGCG AGATGGTGGT GCTGACCTGC GACACCCCCG AGGAGGACGG CATCACCTGG     180
191 ACCCTGGACC AGAGCAGCGA GGTGCTGGGC AGCGGCAAGA CCCTGACCAT CCAGGTGAAG     240
192 GAGTTCGGCG ACGCCGGCCA GTACACCTGC CACAAGGGCG GCGAGGTGCT GAGCCACAGC     300
193 CTGCTGCTGC TGCACAAGAA GGAGGACGGC ATCTGGAGCA CCGACATCCT GAAGGACCAG     360
194 AAGGAGCCCA AGAACAAGAC CTTCCTGCGC TGCGAGGCCA AGAACTACAG CGGCCGCTTC     420
195 ACCTGCTGGT GGCTGACCAC CATCAGCACC GACCTGACCT TCAGCGTGAA GAGCAGCAGG     480
196 GGCAGCAGCG ACCCCCAGGG CGTGACCTGC GGCGCCGCCA CCCTGAGCGC CGAGCGCGTG     540
197 CGCGGCGACA ACAAGGAGTA CGAGTACAGC GTGGAGTGCC AGGAGGACAG CGCCTGCCCC     600
198 GCCGCCGAGG AGAGCCTGCC CATCGAGGTG ATGGTGGACG CCGTCCACAA GCTGAAGTAC     660
199 GAGAACTACA CCAGCAGCTT CTTCATCCGC GACATCATCA GCCCGACCC  CCCCAAGAAC     720
200 CTGCAGCTGA AGCCCCTGAA GAACAGCCGC CAGGTGGAGG TGAGCTGGGA GTACCCCGAC     780
201 ACCTGGAGCA CCCCCCACAG CTACTTCAGC CTGACCTTCT GCGTGCAGGT GCAGGGCAAG     840
202 AGCAAGCGCG AGAAGAAGGA CCGCGTGTTC ACCGACAAGA CCAGCGCCAC CGTGATCTGC     900
203 CGCAAGAACG CCAGCATCAG CGTGCGCGCC CAGGACCGCT ACTACAGCAG CAGCTGGAGC     960
204 GAGTGGGCCA GCGTGCCCTG CAGCTAG                                         987
206 (2) INFORMATION FOR SEQ ID NO: 4:
208     (i) SEQUENCE CHARACTERISTICS:
210         (A) LENGTH: 987 base pairs
211         (B) TYPE: nucleic acid
212         (C) STRANDEDNESS: single
213         (D) TOPOLOGY: linear
215     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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217  ATGTGCCACC AGCAGCTGGT GATCAGCTGG TTCTCCCTGG TGTTTCTGGC CAGCCCCCTC    60
218  GTGGCCATCT GGGAGCTGAA GAAAGACGTG TACGTGGTCG AGCTGGACTG GTACCCCGAC   120
219  GCCCCCGGCG AGATGGTGGT CCTGACCTGC GACACCCCCG AGGAAGACGG CATCACCTGG   180
220  ACCCTGGACC AGAGCAGTGA GGTGCTGGGC TCCGGCAAGA CCCTGACCAT CCAGGTGAAG   240
221  GAGTTCGGCG ACGCCGGCCA GTACACCTGC CACAAGGGAG GCGAGGTGCT GAGCCACTCC   300
222  CTCCTGCTGC TCCACAAAAA GGAGGACGGC ATCTGGAGCA CCGACATCCT GAAGGACCAG   360
223  AAGGAGCCCA AGAACAAGAC CTTCCTGCGC TGCGAGGCCA AGAACTACAG CGGCCGCTTC   420
224  ACCTGCTGGT GGCTGACCAC GATCAGCACC GACCTGACCT TCAGTGTGAA GAGCAGCAGG   480
225  GGCTCCAGCG ACCCCCAGGG CGTGACCTGC GGCGCTGCCA CCCTGAGCGC CGAGCGCGTG   540
226  CGCGGCGACA ACAAGGAGTA CGAGTACAGC GTGGAGTGCC AGGAAGACTC CGCCTGCCCC   600
227  GCCGCTGAGG AGAGCCTGCC CATCGAGGTG ATGGTGGACG CCGTTCACAA GCTGAAGTAC   660
228  GAGAACTACA CCAGCAGCTT CTTCATCCGC GACATCATCA AGCCTGACCC ACCCAAGAAC   720
229  CTCCAGCTGA AGCCCCTCAA GAACTCCCGC CAGGTGGAGG TGAGCTGGGA GTACCCCGAC   780
230  ACCTGGAGCA CGCCCCACTC CTACTTCTCC CTGACCTTCT GCGTGCAGGT CCAGGGCAAG   840
231  AGCAAGCGCG AGAAGAAAGA CCGGGTGTTC ACCGACAAGA CCAGCGCCAC CGTCATCTGC   900
232  CGCAAGAACG CCAGCATCAG CGTGCGCGCC CAGGACCGCT ACTATAGCTC CTCTTGGAGC   960
233  GAGTGGGCCA GCGTGCCCTG CTCCTAG                                       987
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237 (2) INFORMATION FOR SEQ ID NO: 5:
239   (i) SEQUENCE CHARACTERISTICS:
241   (A) LENGTH: 219 amino acids
242   (B) TYPE: amino acid
243   (C) STRANDEDNESS: single
244   (D) TOPOLOGY: linear
246   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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248  Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
249   1               5                   10                  15
251  Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
252                  20                  25                  30
254  Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
255              35                  40                  45
257  Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys
258          50                  55                  60
260  Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
261  65                  70                  75                  80
263  Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys
264              85                  90                  95
266  Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala
267              100                 105                 110
269  Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr
270          115                 120                 125
272  Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys
273      130                 135                 140
274  Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
275  145                 150                 155                 160
277  Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr
278              165                 170                 175
280  Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
281          180                 185                 190
283  Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
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RAW SEQUENCE LISTING   DATE: 01/23/2002
PATENT APPLICATION: US/09/754,014   TIME: 14:37:02

Input Set : N:\Crf3\RULE60\09754014.raw
Output Set: N:\CRF3\01232002\I754014.raw

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284        195              200              205
286  Ile Asp Arg Val Thr Ser Tyr Leu Asn Ala Ser
287        210              215
291  (2) INFORMATION FOR SEQ ID NO: 6:
293        (i) SEQUENCE CHARACTERISTICS:
295             (A) LENGTH: 660 base pairs
296             (B) TYPE: nucleic acid
297             (C) STRANDEDNESS: single
298             (D) TOPOLOGY: linear
300        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
302  ATGTGTCCAG CGCGCAGCCT CCTCCTTGTG GCTACCCTGG TCCTCCTGGA CCACCTCACT    60
303  TTGGCCAGAA ACCTCCCCGT GGCCACTCCA GACCCAGGAA TGTTCCCATG CCTTCACCAC   120
304  TCCCAAAACC TGCTGAGGGC CGTCAGCAAC ATGCTCCAGA AGGCCAGACA AACTCTAGAA   180
305  TTTTACCCTT GCACTTCTGA AGAGATTGAT CATGAAGATA TCACAAAAGA TAAAACCAGC   240
306  ACAGTGGAGG CCTGTTTACC ATTGGAATTA ACCAAGAATG AGAGTTGCCT AAATTCCAGA   300
307  GAGACCTCTT TCATAACTAA TGGGAGTTGC CTGGCCTCCA GAAAGACCTC TTTTATGATG   360
308  GCCCTGTGCC TTAGTAGTAT TTATGAAGAC TTGAAGATGT ACCAGGTGGA GTTCAAGACC   420
309  ATGAATGCAA AGCTTCTGAT GGATCCTAAG AGGCAGATCT TTCTAGATCA AAACATGCTG   480
310  GCAGTTATTG ATGAGCTGAT GCAGGCCCTG AATTTCAACA GTGAGACTGT GCCACAAAAA   540
311  TCCTCCCTTG AAGAACCGGA TTTTTATAAA ACTAAAATCA AGCTCTGCAT ACTTCTTCAT   600
312  GCTTTCAGAA TTCGGGCAGT GACTATTGAC AGAGTGACGA GCTATCTGAA TGCTTCCTAA   660
316  (2) INFORMATION FOR SEQ ID NO: 7:
318        (i) SEQUENCE CHARACTERISTICS:
320             (A) LENGTH: 660 base pairs
321             (B) TYPE: nucleic acid
322             (C) STRANDEDNESS: single
323             (D) TOPOLOGY: linear
325        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
327  ATGTGCCCCG CCCGCAGCCT GCTGCTGGTG GCCACCCTGG TGCTGCTGGA CCACCTGAGC    60
328  CTGGCCCGCA ACCTGCCCGT GGCCACCCCC GACCCCGGCA TGTTCCCCTG CCTGCACCAC   120
329  AGCCAGAACC TGCTGGCGGC CGTGAGCAAC ATGCTGCAGA AGGCCGCGCA GACCCTGGAG   180
330  TTCTACCCCT GCACCAGCGA GGAGATCGAC CACGAGGACA TCACCAAGGA CAAGACCAGC   240
331  ACCGTGGAGG CCTGCCTGCC CCTGGAGCTG ACCAAGAACG AGAGCTGCCT GAACAGCCGC   300
332  GAGACCAGCT TCATCACCAA CGGCAGCTGC CTGGCCAGCC GCAAGACCAG CTTCATGATG   360
333  GCCCTGTGCC TGAGCAGCAT CTACGAGGAC CTGAAGATGT ACCAGGTGGA GTTCAAGACC   420
334  ATGAACGCCA AGCTGCTGAT GGACCCCAAG CTCCAGATCT TCCTGGACCA GAACATGCTG   480
335  GCCGTGATCG ACGAGCTGAT GCAGGCCCTG AACTTCAACA GCGAGACCGT GCCCCAGAAG   540
336  AGCAGCCTGG AGGAGCCCGA CTTCTACAAG ACCAAGATCA AGCTGTGCAT CCTGCTGCAC   600
337  GCCTTCCGCA TCCGCGCCGT GACCATCGAC CGCGTGACCA GCTACCTGAA CGCCACCTGA   660
342  (2) INFORMATION FOR SEQ ID NO: 8:
344        (i) SEQUENCE CHARACTERISTICS:
346             (A) LENGTH: 660 base pairs
347             (B) TYPE: nucleic acid
348             (C) STRANDEDNESS: single
349             (D) TOPOLOGY: linear
351        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
353  ATGTGCCCCG CCCGCAGCCT GCTGCTCGTG GCCACCCTGG TGCTCCTGGA CCACCTCAGC    60
354  CTGGCCCGCA ACCTCCCCGT GGCCACCCCA GACCCCGGCA TGTTCCCATG CCTGCACCAC   120
355  AGCCAGAACC TGCTGGCGGC CGTGAGCAAC ATGCTGCAGA AGGCCGCGCA GACCCTGGAG   180
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VERIFICATION SUMMARY   DATE: 01/23/2002
PATENT APPLICATION: US/09/754,014   TIME: 14:37:03

Input Set : **N:\Crf3\RULE60\09754014.raw**
Output Set: **N:\CRF3\01232002\I754014.raw**

L:40 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:41 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]